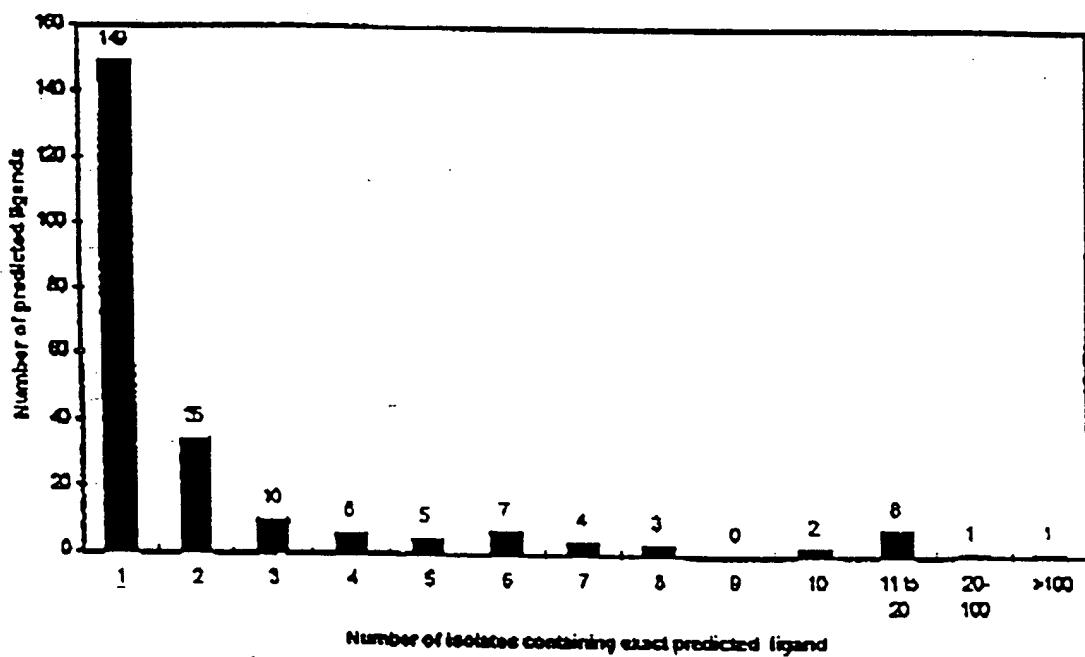


FIG. 1

a)



b)

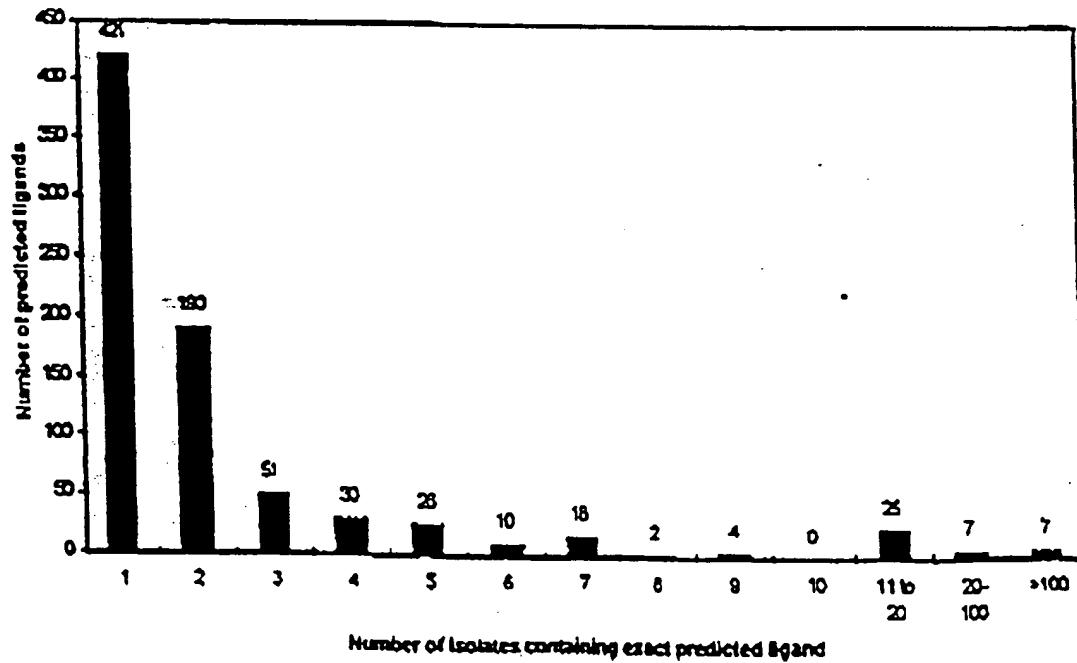
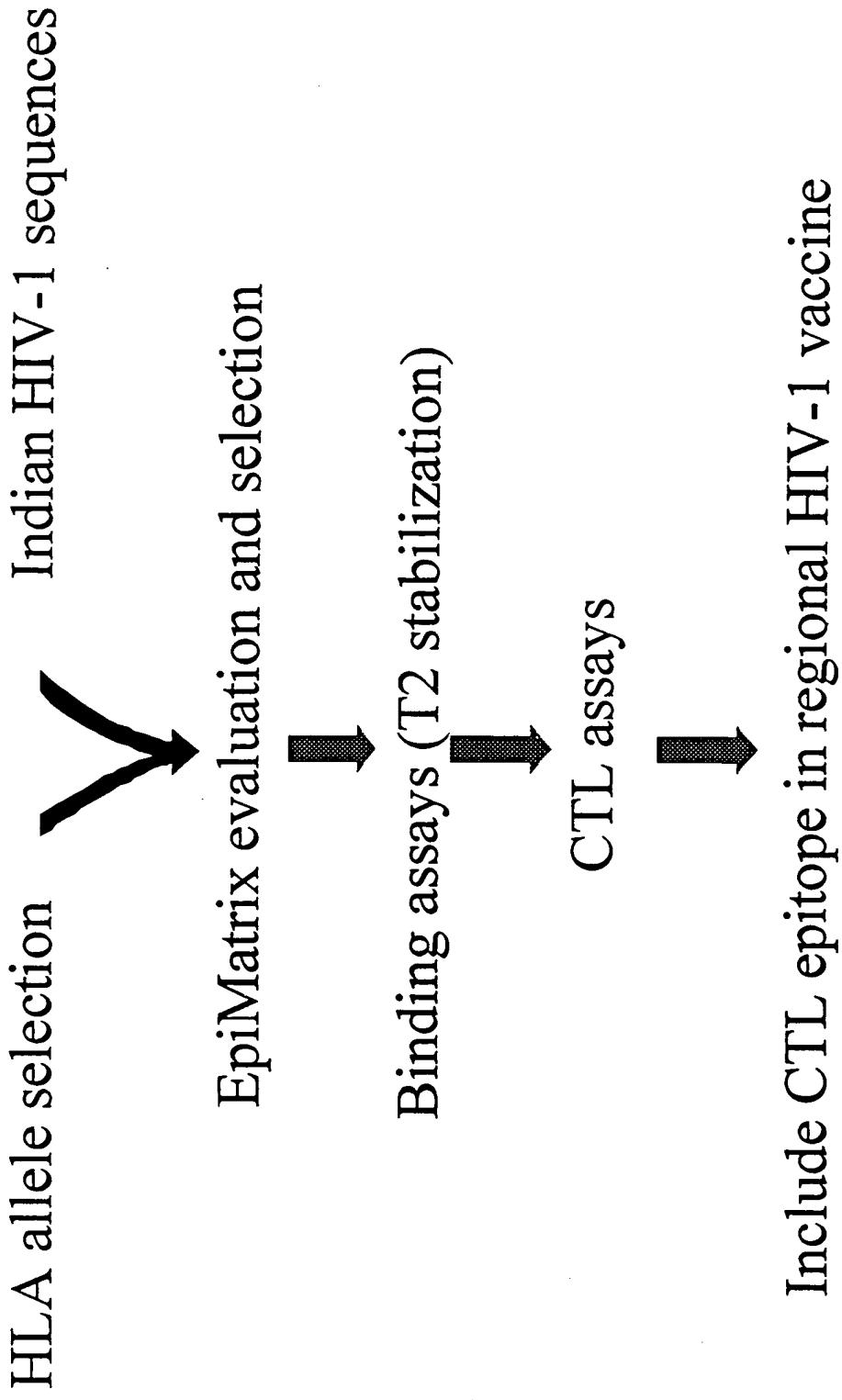


FIG. 2

Sequence	A2 EBP	B27 EBP	A2 Fold Increase (less than 1.3 not reported)	B27 Fold Increase (less than 1.3 not reported)	Protein	Number of Isolates with Exact A.A.	Approximate Position in LAI sequence	Clade			Clade D	Clade E	Other SEQ ID NO.
								A	B	C			
KLTPLCVTLN	55.68%	0.00%	1.33		Env	159	gp120 - 120	X	X	X	X	X	1
AEWDRVHPV	66.42%	0.00%	1.35		Gag	36	gag - 215	X	X	X	X	X	2
SLFNTVATL	62.00%	0.00%			Gag	18	gag - 100	X	X	X	X	X	3
ELHPDKWTY	57.03%	0.00%			RT	17	RT - 354	X	X	X	X	X	4
GMDPDEREVL	72.52%	0.00%	2.7		Nef	17	nef - 170	X	X	X	X	X	5
GMDDPEKEVL	87.51%	0.01%	1.33		Nef	16	nef - 170	X	X	X	X	X	6
HLWRWGTMIL	76.69%	0.00%			Env	10	gp120 - 30	X	X	X	X	X	7
LLLTRDGGVN	55.68%	0.00%			Env	>10	gp120 - 452	X	X	X	X	X	8
HLWKWSTMIL	90.92%	0.00%	1.63		Env	>10	gp120 - 20	X	X	X	X	X	9
ILKEPVHGV	97.47%	0.00%	1.54		RT	>10	RT - 480	X	X	X	X	X	10
KRWILGLNK	0.00%	14.22%	3.61		Gag	79	gag - 263	X	X	X	X	X	11
CRIKQIN	0.00%	99.08%			Env	185	gp120 - 420	X	X	X	X	X	12
CRIKQINMW	0.00%	99.52%	1.74		Env	150	gp120 - 420	X	X	X	X	X	13
VSFEPPIHF	0.20%	55.61%	1.45		Env	109	gp120 - 215	X	X	X	X	X	14
RCSNNITGL	0.01%	62.11%			Env	101	gp120 - 446	X	X	X	X	X	15
VSFEPPIHY	0.00%	98.22%			Env	101	gp120 - 215	X	X	X	X	X	16
CRIKQIVNM	0.00%	91.33%			Env	75	gp120 - 420	X	X	X	X	X	17
IRSENITNN	0.00%	82.77%			Env	42	gp120 - 275	X	X	X	X	X	18
IRFIMIV	0.05%	89.06%			Env	19	gp41 - 175	X	X	X	X	X	19
ISFDPPHY	0.01%	67.49%			Env	15	gp120 - 215	X	X	X	X	X	20
YRTGDDIG	0.00%	56.14%			Env	15	gp120 - 330	X	X	X	X	X	21
IRIGPGQTIFY	0.07%	75.36%			Env	13		X	X	X	X	X	22
GCGGKJIC	0.00%	61.09%			Env	12	gp41 - 90	X	X	X	X	X	23
RRRAPQDS	0.00%	67.49%			Tat	12		X	X	X	X	X	24
IRSENITDN	0.00%	59.28%			Env	11	gp120 - 275						25
CRIKQFIN	0.00%	76.92%	1.53		Env	<10	gp120 - 420	X	X	X	X	X	26
KRISIGPGR	0.00%	56.93%	1.78		Env	<10	gp120 - 320	X	X	X	X	X	27
GCQQTEQL	0.10%	78.95%			Env	<10	gp41 - 270	X	X	X	X	X	28
GRRGWEILKY	0.01%	59.80%	3.27		Env	<10	gp41 - 270	X	X	X	X	X	29

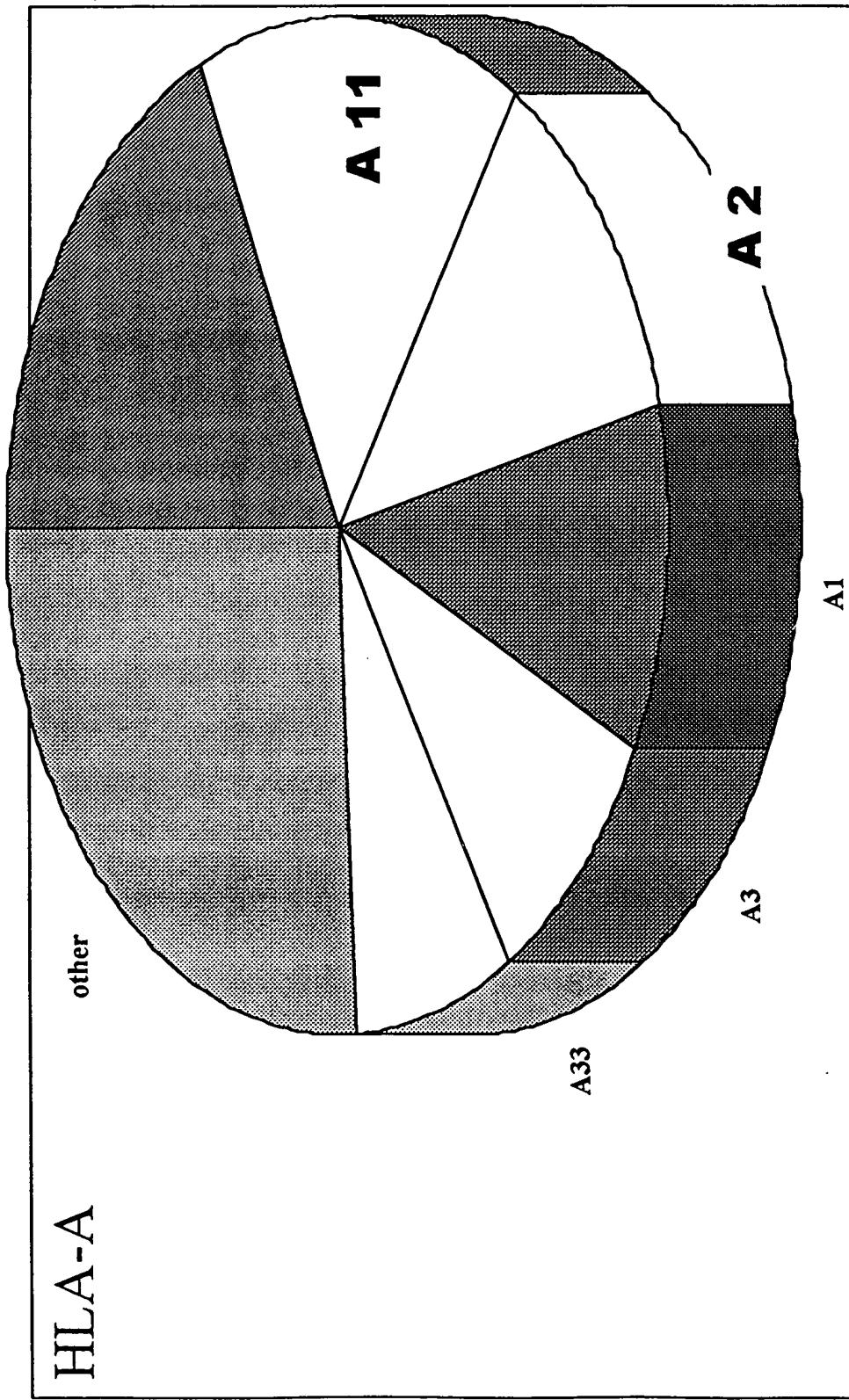
FIG. 3

Project Outline



**Methods: HLA allele selection**

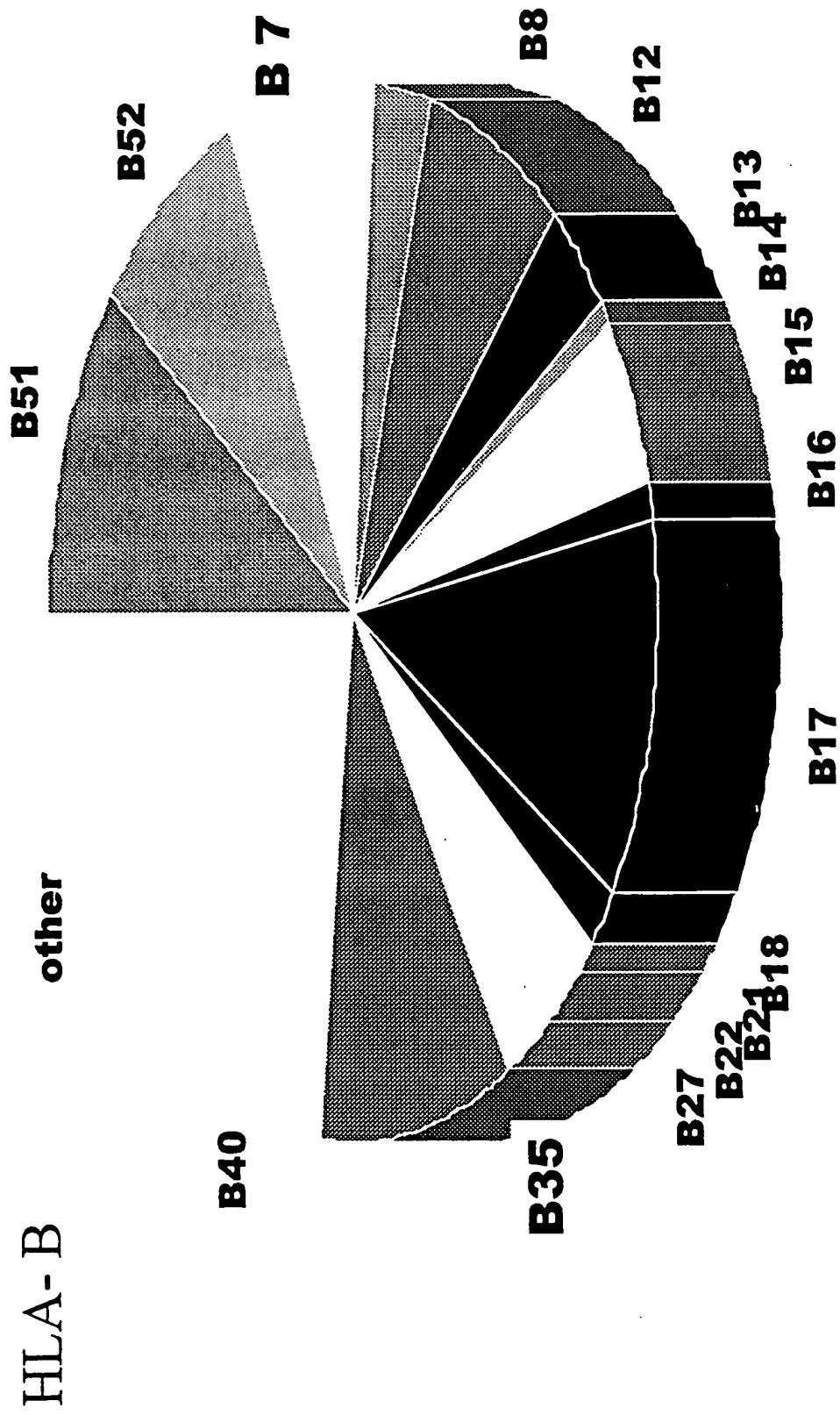
FIG. 4



HLA-A2 and -A11, -B7 and -B35 were selected for this pilot project due their prevalence of the HLA alleles in the Indian population....

FIG. 5

Methods: HLA allele selection



... and availability of cell lines for *in vitro* study.

FIG. 6  
EpiMatrix Predictions and Binding Results: B 7  
6 out of 7, and control peptide

B7		p ptid #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBF	avg MFI (200ug/ml)	avg f Id incr. (20ug/
1		RPNNNNTRKSI	RPNNNNTRKSI	ENV	DID757	183-192	75	Y	8%	335.6	2.4	
3		NPYNTPIFAL	NPYNTPIFAL	POL	SolInd5	61-70	60		20%	281.9	2.0	
4		RAIEQQHLL	RAIEAQHLL	ENV	DID747	481-490	60		17%	181.5	1.3	
5		TCKSNITGLL	TCKSNITGLL	ENV	DID760	375-384	59		18%	160.5	1.2	
		KPVVSTQLL	KPVVSTQLL	ENV	DID747	182-191	71		46%	248.5	1.8	
		KPCVKLTPLC	KPCVKLTPLC	ENV	DID747	51-60	100		27%	373.8	2.7	
		GPKVKQWPL	GPKVKQWPL	POL	SolInd4	25-34	100		27%	314.7	2.3	
		YPGIKVRQL	YPGIKVRQL	POL	SolInd4	278-287	100		26%	378.4	2.7	

FIG. 7  
EpiMatrix Predictions and Binding Results: B 35  
7 out of 7 ... and control peptide

B37							
Peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL predicted EBF
2	TVLDVGDAYF	TVLDVGDAYF	POL	Solnd4	114-123	100	Y
6	EPPFLWMGY	EPPFLWMGY	POL	Solnd4	231-239	100	9%
7	VPVKLKPGM	VPVKLKPQMD	POL	Solnd4	15-24	100	9%
8	CPKVTFDPI	CPKVTFDPIP	ENV	DiD760	144-153	53	7%
	KPVVSTQLL	KPVVSTQLL	ENV	DiD747	182-191	71	9%
	KPCVKLTPL	KPCVKLTPL	ENV	DiD747	51-60	100	11%
	GPKVKQWPPL	GPKVKQWPPL	POL	Solnd4	25-34	100	11%
	YPGIKVRLQL	YPGIKVRLQL	POL	Solnd4	278-287	100	7%

FIG. 8  
EpiMatrix Predictions and Binding Results: A 2  
3 out of 7 ... and control peptide

A2									
peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBF	avg MFI (200ug/ml) avg f Id incr. (20ug/ml)
13	ILKEPVHGV	ILKEPVHGVY	POL	Solnd4	316-325	80	Y	96%	1604.2
14	QLPEKDSWTV	QLPEKDSWTV	POL	Solnd4	252-261	100		87%	1368.1
15	NLWTVYYGV	NLWTVYYGV	ENV	GID1024	32-41	67		84%	1716.9
16	QMHEDEVSL	QMHEDEVSLW	ENV	DiD747	37-46	91		78%	1413.1
17	KIEELREHLL	KIEELREHLL	POL	Solnd5	208-217	60		79%	889.9
18	DMVNQMHEDV	DMVNQMHEDV	ENV	DiD747	33-42	64		77%	731.1
19	GLKKKKSVTV	GLKKKKSVTV	POL	Solnd4	106-115	100		76%	1088.4
20	ELHPDKWTV	ELHPDKWTVQ	POL	Solnd4	240-249	80		72%	1048.1

FIG. 9  
EpiMatrix Predictions and Binding Results: A 11  
4 out of 7 ... and control peptide

A'11									
P Pptide #	peptide	seq.	Used	gene	strain	start-stop	% conserved	CTL	predicted EBFI
21	IYQEPFKNLK	IYQEPFKNLK	POL	SolInd4	348-357	100	Y	7%	677.5
22	VTFDPIHY	VTFDPIHY	ENV	DID760	147-156	53		22%	190.0
23	TVQQCTHGIK	TVQQCTHGIK	ENV	DID747	174-183	59		44%	733.4
24	NTPIFALKKK	NTPIFALKKK	POL	SolInd5	64-73	60		44%	187.8
25	LVDFRELNK	LVDFRELNK	POL	SolInd4	81-90	100		47%	755.2
26	PGMDGPKVK	PGMDGPKVK	POL	SolInd4	21-30	100		52%	193.8
27	GIPHPAGLKK	GIPHPAGLKK	POL	SolInd4	100-109	100		62%	309.6
28	FTTPDKKKHQK	FTTPDKKKHQK	POL	SolInd4	221-330	100		63%	920.6

FIG. 10  
Methods: T2 Binding Assay

Allele matched peptides stabilize MHC molecules on the surface of TAP deficient cells. The stabilized MHC-peptide complex is detected using Ab to the MHC and fluorescence labeled secondary Ab.

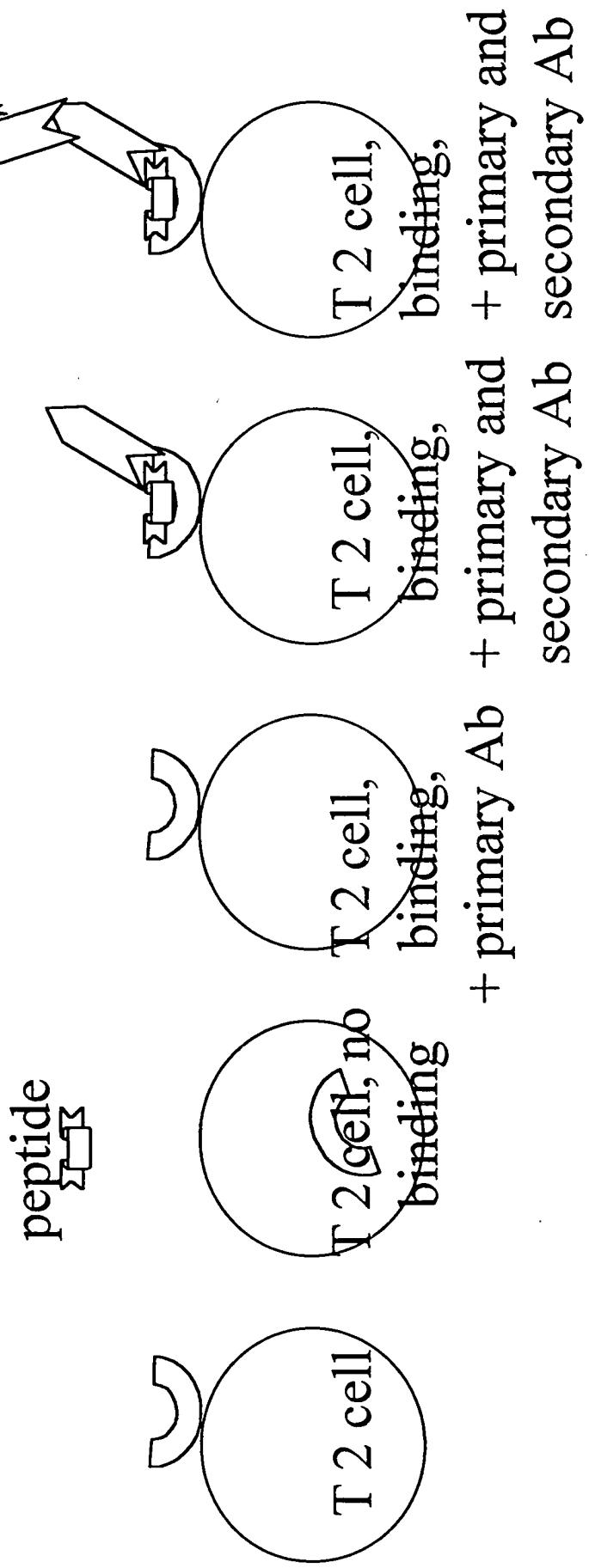
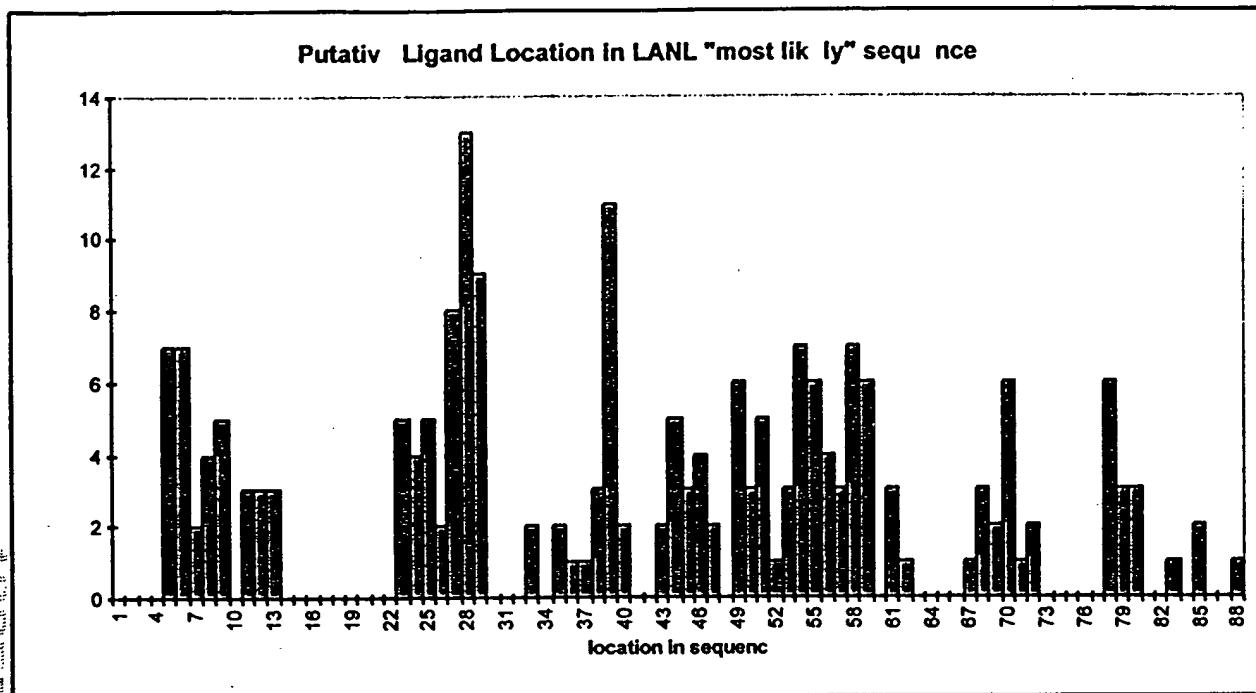


FIG. 11  
Clustering of putative MHC ligands in *env*



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